

### REMARKS

Claims 1, 2-4, 10-11 and 23 remain in the application. Only Claims 1, 12 and 23 are in independent form. Reconsideration of the subject application as amended pursuant to and consistent with 37 C.F.R. §1.112 and in light of the remarks which follow are respectfully requested.

With the present response Applicants have corrected typographical errors found in the specification. Applicants enclose a set of modified pages of the description for the benefit of the Examiner.

Applicants have also corrected obvious errors found in the specification. A marked-up version of the changes made to the specification are found in the "Version with markings to show changes made" attached to this paper. The following clarifications are provided for the Examiner's benefit:

a) The error contained at page 4 line 24.

Point N°14 was referring to itself. This point thus obviously contains an error. Point 14 refers to a recombinant polypeptide. Point N°13 page 4 line 21 refers to a purified or isolated recombinant polypeptide comprising the amino acid sequence of secreted soluble  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3 or  $\alpha_2\delta$ -4 subunit polypeptide. By reading the specification it is obvious that point N°14 should refer to point N°13.

b) The error contained at page 20 line 26.

Page 20 line 26 relates to a polypeptide comprising an amino acid sequence having particular percentage of identity with cited amino acid sequences under which are SEQ ID N°4-6, SEQ ID N°10-12, SEQ ID N°16-17. However it refers to SEQ ID N°19 which is a DNA sequence corresponding to full length  $\alpha_2\delta$ -2. This paragraph thus obviously contains an error. By reading the specification it is obvious that this paragraph should refer to SEQ ID N°18. This obvious correction is further demonstrated by the reading of page 20 line 34 of the specification which mentions SEQ ID N°4-6, SEQ ID N°10-12 and SEQ ID N°16-18 as being preferred amino acids sequences of the invention.

c) The error contained at page 31 line 20 and 25.

Example 11 relates to a nucleotide sequence encoding a soluble secreted mouse  $\alpha_2\delta$ -3 deletion mutant of cited amino acid sequence. However it refers to SEQ ID N°25 which is a DNA sequence. This example thus obviously contains an error. By reading the specification it is obvious that this paragraph should refer to SEQ ID N°24. This obvious correction is further demonstrated by the reading of page 33 line 9-10.

In the following paragraph, Applicants first provide a summary of some of the key points of the present invention. This is followed by comments to the specific rejections set forth in the Office Action.

The invention relates to truncated  $\alpha_2\delta$  calcium channel subunit cDNA sequences which encode soluble secreted polypeptides which lack a C-terminal portion of the corresponding native protein while retaining their calcium channel subunit properties.

The term "soluble secreted  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3 or  $\alpha_2\delta$ -4 subunit" is intended to designate polypeptide sequences which, when produced by a recombinant host cell, are secreted at least partially into the culture medium rather than remaining associated with the host cell membrane (see the specification at page 8 lines 5-9).

Full length  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3 or  $\alpha_2\delta$ -4 subunits are membrane associated and thus are not secreted soluble. Therefore full length  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3 or  $\alpha_2\delta$ -4 subunits are not part of the invention.

Preferably the secreted soluble  $\alpha_2\delta$  calcium channel subunit are human  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3 or  $\alpha_2\delta$ -4 polypeptides. However, due to cross species homology for the  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3 or  $\alpha_2\delta$ -4 subunit, the C-terminal deletion may also be applied to other eukaryotic species.

The present application specifically discloses the following deletion mutants:

For human  $\alpha_2\delta$ -2:

- a 1062 amino acid long mutant (see nucleic sequence SEQ ID N°1 and amino acid sequence SEQ ID N°4)
- a 1082 amino acid long mutant (see nucleic sequence SEQ ID N°2 and amino acid sequence SEQ ID N°5)
- a 1109 amino acid long mutant (see nucleic sequence SEQ ID N°3 and amino acid sequence SEQ ID N°6).

For human  $\alpha_2\delta$ -3:

- a 1019 amino acid long mutant (see nucleic sequence SEQ ID N°7 and amino acid sequence SEQ ID N°10)
- a 1038 amino acid long mutant (see nucleic sequence SEQ ID N°8 and amino acid sequence SEQ ID N°11)
- a 1065 amino acid long mutant (see nucleic sequence SEQ ID N°9 and amino acid sequence SEQ ID N°12).

For human  $\alpha_2\delta$ -4:

- a 304 amino acid long mutant (see nucleic sequence SEQ ID N°13 and amino acid sequence SEQ ID N°16)
- a 323 amino acid long mutant (see nucleic sequence SEQ ID N°14 and amino acid sequence SEQ ID N°17)
- a 350 amino acid long mutant (see nucleic sequence SEQ ID N°15 and amino acid sequence SEQ ID N°18).

The use of some of these mutants is further illustrated through the examples referring to SEQ ID N°23 which is a truncated  $\alpha_2\delta$ -2 which corresponds to a 1109 amino acid long mutant to which a 6His tag has been added and the example relating to SEQ ID N°24 which is a  $\alpha_2\delta$ -3 deletion mutant to which a 6His tag has been added.

Claims 1, 9 and 12 stand rejected under 35 U.S.C §112, first paragraph, because the specification, while enabling for nucleotides encoding SEQ ID NO: 20 and 22, does not reasonably provide enablement for a nucleic acid encoding any other polypeptide.

The objection against Claim 9 can now be withdrawn since this claim has been deleted.

With regard to Claims 1 and 12, Applicants respectfully submit that these claims refer to secreted soluble polypeptides of  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3,  $\alpha_2\delta$ -4 subunit. It is to be noted that SEQ ID NO: 20 and SEQ ID NO: 22 refer to full length sequences and do not fall into the scope of Claim 1.

Truncated  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3,  $\alpha_2\delta$ -4 subunits have been illustrated by 3 specific sequences respectively. The one skilled in the art has enough guidance to create other deletion mutants which are secreted soluble  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3 or  $\alpha_2\delta$ -4 subunit polypeptides which retain their voltage-dependent calcium channel properties. Experimentation will be necessary to determine the interest of using shorter or longer mutants but the skilled person has an expectation of success based on the initial guidance of the specification and hence no undue experimentation is necessary.

In view of the above, withdrawal of the rejection of Claims 1, 9 and 12 under 35 USC §112, first paragraph is respectfully requested.

Claims 2-3 and 5 stand rejected under 35 U.S.C §112, first paragraph, because the specification while being enabling for a polynucleotide encoding a substantially purified polypeptide comprising an amino acid sequence set forth in SEQ ID NO: 20 and 22, does not reasonably provide enablement for a polynucleotide encoding a substantially purified variant having at least 90% amino acids sequence identity to SEQ ID NO 20 and 22. The specification does not enable any person skilled in the art to which it pertains or with which it is most nearly connected to make and use the invention commensurate in scope with these claims.

The objection against Claim 5 can now be withdrawn since this claim has been deleted.

In response, Applicants wish to point out that Claims 2 and 3 have been amended to clarify the types of amino acids substitutions which can be contemplated by the skilled person.

Amended Claim 2 is supported by the specification at page 20, line 36 to the end of page 21.

Amended Claim 3 is supported by the specification at page 20, line 36 to the end of page 21.

In view of amended Claims 2 and 3, withdrawal of the rejection of those claims under 35 USC §112, first paragraph is respectfully requested.

Claims 1, 7, 9 and 12 stand rejected under 35 USC §112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicants regards as the invention.

The Examiner indicates that Claims 1, 9 and 12 are indefinite in that they only describe the peptide of interest by an arbitrary protein name, i.e., "alpha2delta-2" and that nothing in the claims distinctly identifies the protein.

The objection against Claim 9 can now be withdrawn since this claim has been deleted.

In response, Applicants wish to point out that protein names  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3,  $\alpha_2\delta$ -4 are definite, per se, for one of ordinary skill in the art. As an example, Klugbauer et al. (The Journal of Neuroscience, January 15, 1999, 19(2): 684-691) describe two forms of the full length calcium channel  $\alpha_2\delta$ -2 subunit and one form of the full length calcium channel  $\alpha_2\delta$ -3 subunit. Thus, the wording  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3,  $\alpha_2\delta$ -4 provide adequate guidance as to the nature of the polypeptide which Applicants claim.

Furthermore, Applicants wish to point out that the  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3,  $\alpha_2\delta$ -4 subunit polypeptides of the invention are defined as mammalian secreted soluble cerebral cortical voltage-dependent calcium channel subunit polypeptides. Thus Claims 1, 9 and 12 distinctly claim the subject matter of the invention.

In view of the above, withdrawal of the rejection of Claims 1, 9 and 12 under 35 USC §112, second paragraph, is respectfully requested.

The Examiner also indicates that Claims 7 and 9 are indefinite because they recite the term "stringent conditions" which is a conditional term and because some nucleic acids which might hybridize under conditions of moderate stringency for example would fail to hybridize under conditions of high stringency.

The objection against Claims 7 and 9 can now be withdrawn since these claims have been deleted.

Claims 1, 4 and 10-12 stand rejected under 35 USC §102(b). The Examiner explains that Wei et al. disclose a human  $\alpha_2$  calcium channel which is 100% identical to SEQ ID NO: 1.

In response Applicants provide herewith as Exhibit 1 a sequence alignment of the human  $\alpha_2$  calcium channel sequence disclosed in Wei et al. and SEQ ID NO: 1 disclosed in the present application.

This alignment shows that Wei et al. disclose a full length human  $\alpha_2\delta$ -2 subunit polypeptide (5463 nucleotides (AF042792)) whereas SEQ ID NO: 1 of the present application is a truncated version of this full length polypeptide (3186 nucleotides). Thus the sequence of the  $\alpha_2$  calcium channel disclosed by Wei et al. is not the same sequence as sequence SEQ ID NO: 1. Therefore, the  $\alpha_2$  calcium channel disclosed by Wei et al. is not 100% identical to the sequence of SEQ ID NO: 1. Furthermore it is clear from this

analysis that Wei et al. does not disclose any form of truncated calcium channel subunit. Hence Claims 1, 4, 10-12 are novel over this prior art.

The amendment of Claim 4 results from a typographical error. Appropriate sequences to be incorporated in this claim are provided at page 10, lines 16-19 of the specification as filed.

In view of the arguments set forth above withdrawal of the rejection of Claims 1, 4 and 10-12 under 35 USC §102(b) is respectfully requested.

Claims 1, 6, 7 and 9-12 are rejected under 35 USC §102(b) as being anticipated by WO9504822.

The objection against Claims 6, 7 and 9 can now be withdrawn since those claims have been deleted.

The Examiner explains that Harpold et al. disclose the cloning and expression of human voltage gated calcium channel subunits thus anticipating Claim 1.

In response, Applicants wish to draw the attention of the Examiner to the fact that Claim 1 refers to secreted soluble voltage-dependent calcium channel  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3,  $\alpha_2\delta$ -4 subunit polypeptides and not only to voltage gated  $\text{Ca}^{2+}$  subunits. Therefore, Harpold et al. do not disclose a purified or isolated nucleic acid encoding a mammalian secreted soluble cerebral cortical voltage-dependent calcium channel  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3 or  $\alpha_2\delta$ -4 subunit polypeptide of Claim 1.

In conclusion Claim 1 is not anticipated by Harpold et al.

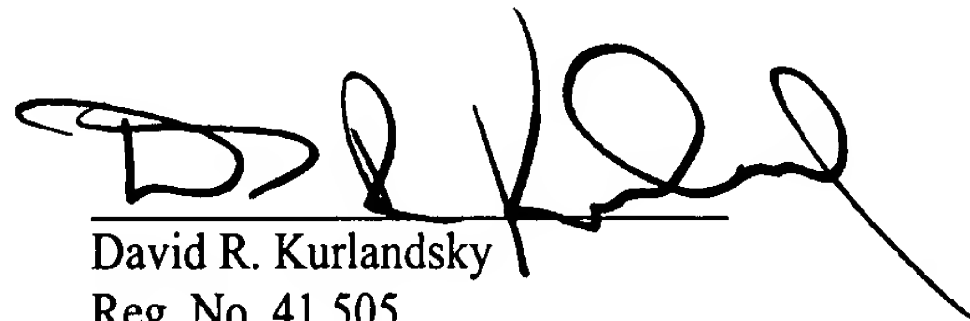
In view of the arguments set forth above withdrawal of the rejection of Claims 1, 6, 7 and 9 under 35 USC §102(b) is respectfully requested.

In view of the foregoing, further and favorable action in the form of a Notice of Allowance is believed to be next in order, and such action is earnestly solicited.

The Commissioner is hereby authorized to charge any fees under 37.C.F.R §1.116 and 1.117 that may be required by this paper to Deposit Account No. 23-0455.

In the event the Examiner wishes to discuss any matter concerning this application, he is invited to communicate with the undersigned.

Respectfully submitted,

A handwritten signature in black ink, appearing to read 'D. R. Kurlandsky', written over a horizontal line.

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Attachment - Amendments to the specification and claims, Version with markings to show changes made  
Exhibit 1

DK1P4407.doc



**"Version with markings to show changes made."**

**IN THE SPECIFICATION:**

Please correct the following typographical errors:

At page 2, second paragraph:

The only assay currently available for the screening of ligands that bind the  $\alpha_2\delta$  subunit involves the use of pig membrane extracts as a source of the  $\alpha_2\delta$  subunit. Such an assay presents major inconvenients. Firstly, [bcause] because the assay material is a membrane extract, it is very difficult to accurately determine the protein composition from one assay preparation to another particularly with regard to the subtype. Also, the presence of various impurities in the assay preparation is a problem in small plate assays. Furthermore, as the protein preparation lacks homogeneity, the interaction between the targeted protein and the assay plate is often quite uneven. This [rendres] renders the streamlining of the assay in a high throughput format almost impossible to achieve.

At page 4, sixth paragraph:

14) A recombinant polypeptide according to [14)] 13), having at least 80% amino-acid identity with a polypeptide comprising:

- from amino acid 1 to between amino acids 1027 and 1062 of the amino acid sequence of SEQ ID N°20, or
- from amino acid 1 to between amino acids 1019 and 1079 of the amino acid sequence of SEQ ID N°22.

At page 9, first paragraph:

their native folding and hence [thir] their [<sup>3</sup>H]gabapentin binding properties are those corresponding to the native protein in which amino-acid stretch \_\_984\_\_ to \_\_C-terminal end\_\_ of the amino-acid sequence of SEQ ID N°22 has been deleted. The skilled scientist can quite easily determine within this amino-acid stretch the optimal  $\alpha_2\delta$ -3 subunit polypeptides.

At page 10, second full paragraph:

(a) a purified or isolated nucleic acid encoding [a] a secreted soluble  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3 or  $\alpha_2\delta$ -4 subunit having at least 80% amino acid identity with the polypeptide of SEQ ID N°20 or 22, or a sequence complementary thereto;

At page 18, second paragraph:

Once the optimal radioligand binding conditions have been determined, a test ligand can be introduced in the assay medium to evaluate the level of displacement of the radioligand. The concentration of test ligand to be introduced in the assay medium usually varies from 0.1 nM to about 100 [uM]  $\mu$ M. A preferred test ligand concentration of about 10 [uM]  $\mu$ M is usually a starting point in a high throughput screening assay. Then, depending on the number of hits obtained, it may be lowered or increased.

At page 18, sixth paragraph:

The interaction of the secreted soluble  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3 or  $\alpha_2\delta$ -4 subunit polypeptide with the flashplates can be optimized by adjusting the concentration of the polypeptide and by introducing a reagent which will favor this interaction. When a standard NEN Ni chelate flashplate is used, the secreted soluble  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3 or  $\alpha_2\delta$ -4 subunit polypeptide volume usually varies between 0.5 and 20 [ul]  $\mu$ l for a concentration of secreted soluble  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3 or  $\alpha_2\delta$ -4 subunit polypeptide of 0.6 [pmol/ul] pmol/ $\mu$ l. As the published maximum binding capacity of

At page 19, first paragraph:

NEN p plates is about 6 pmol per well, the inventors consider that an optimal concentration of secreted  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3 or  $\alpha_2\delta$ -4 subunit polypeptide is probably around 5 pmol per well at 8 [ul]  $\mu$ l.

At page 19, second paragraph:

With regard to the reagent favoring the interaction between the secreted soluble  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3 or  $\alpha_2\delta$ -4 subunit polypeptide and the radioligand as well as the flashplates, the inventors believe that imidazole could also be efficiently used for that purpose when the secreted soluble  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3 or  $\alpha_2\delta$ -4 subunit polypeptide is tagged with an amino acid sequence including 6 histidine residues. The inventors also believe that imidazole concentrations can substantially [enhanced] enhance binding of the radioligand to the secreted soluble  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3 or  $\alpha_2\delta$ -4 polypeptide. The optimal concentration of imidazole used to enhance radioligand binding varies depending on the concentration of secreted soluble  $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3 or  $\alpha_2\delta$ -4 subunit polypeptide used in the assay. For instance, when the volume of the  $\alpha_2\delta$ -1 subunit polypeptide is about 10 [ul ul]  $\mu$ l ( $\alpha_2\delta$ -2,  $\alpha_2\delta$ -3 or  $\alpha_2\delta$ -4 polypeptide concentration of 0.6 [pmol/ul] pmol/ $\mu$ l), the optimal imidazole concentration can vary between 1 and 20 mM, with a concentration of about 10 mM being preferred. As mentioned previously, other compounds such as histidine as well as pH variations may be used to enhance radioligand binding.

At page 19, fourth paragraph:

Once the optimal radioligand binding conditions have been determined, a test ligand can be introduced in the assay medium to evaluate the level of displacement of the radioligand. The concentration of test ligand to be introduced in the assay medium usually varies from 0.1 nM to about 100 [uM]  $\mu$ M. A preferred test ligand concentration of about 10 [uM]  $\mu$ M is usually a

At page 20, fifth paragraph:

In a further preferred embodiment, the polypeptide comprises an amino acid sequence having at least 80%, preferably 90%, more preferably 95%, and most preferably 98% or 99% amino acid identity with the amino acid sequence of SEQ ID N°4, SEQ ID N°5, SEQ ID N°6, SEQ ID N°10, SEQ ID N°11, SEQ ID N°12, SEQ ID N°16, SEQ ID N°17 and [SEQ ID N°19] SEQ ID N°18.

At page 29, fourth paragraph:

**Example 8**

**Ni Flashplate assay of [<sup>3</sup>H]Leucine binding to secreted soluble human  $\alpha_2\delta$ -2-6His**

The procedure described in example 7 is repeated, except that [<sup>3</sup>H]gabapentin is replaced by 25 [ul]  $\mu$ l (10.1 nM) of [<sup>3</sup>H]Leucine (41 Ci/mmol).

At page 30, first indentation under **Example 9**:

25 $\mu$ l 10 mM HEPES pH7.4 or 25 [ul othe]  $\mu$ l of the test  
compound at the appropriate concentration in HEPES

At page 31, third paragraph:

**Example 11**

**Construction of a nucleotide sequence encoding a soluble secreted mouse  $\alpha_2\delta$ -3 deletion mutant of SEQ ID N°25 as follows.**

**a) Primer design**

PCR primers were designed to generate the secreted soluble mouse  $\alpha_2\delta$ -3 deletion mutant of [SEQ ID N° 25] SEQ ID N°24 as follows:

IN THE CLAIMS:

Please amend Claims 2, 3 and 4 as follows:

Claim 2 (amended). A purified or isolated nucleic acid according to claim 1, comprising a polynucleotide having at least 90% identity with the sequence encoding :

- from amino-acid 1 to between amino-acids 1027 and 1062 of SEQ ID N°20 for  $\alpha_2\delta$ -2,
- from amino-acid 1 to between amino-acids 984 and 1019 of SEQ ID N°22 for  $\alpha_2\delta$ -3

wherein the differing nucleotides encode amino acids which are the same as the amino acids of the SEQ ID N°20 and SEQ ID N°22 through codon degeneracy or encode amino acids which are equivalent to the amino acids of SEQ ID N°20 and SEQ ID N°22 either by structural homology, by net charge or hydrophobicity similarity, such that the encoded polypeptide retains its specificity and affinity properties to the biological targets of the parent polypeptides.

Claim 3 (amended). A purified or isolated nucleic acid according to claim 1, having at least 90% identity with the sequence encoding :

- from amino-acid 1 to between amino-acids 1047 and 1062 of SEQ ID N°20 for  $\alpha_2\delta$ -2,
- from amino-acid 1 to between amino-acids 1004 and 1019 of SEQ ID N°22 for  $\alpha_2\delta$ -3

wherein the differing nucleotides encode amino acids which are the same as the amino acids of the SEQ ID N°20 and SEQ ID N°22 through codon degeneracy or encode amino acids which are equivalent to the amino acids of SEQ ID N°20 and SEQ ID N°22 either by structural homology, by net charge or hydrophobicity similarity, such that the encoded polypeptide retains its specificity and affinity properties to the biological targets of the parent polypeptides.

Claim 4 (amended). A purified or isolated nucleotide sequence according to claim 1 wherein said sequence is the sequence of SEQ ID N°1, SEQ ID N°2, SEQ ID N°3, SEQ ID N°7, SEQ ID N°8, SEQ ID N°9, SEQ ID N°13, SEQ ID N°14, or SEQ ID N°15[, SEQ ID N°19 or SEQ ID N°21].

Please delete Claims 5, 6, 7 and 9.

Please add new Claim 23.

Claim 23 (NEW). A purified or isolated nucleic acid having at least 90% identity with the nucleotide sequence of SEQ ID N°1, SEQ ID N°2, SEQ ID N°3, SEQ ID N°7, SEQ ID N°8, SEQ ID N°9, SEQ ID N°13, SEQ ID N°14, or SEQ ID N°15.

Exhibit 1  
Sequence alignment of sequence SEQ ID N°1 of the patent  
application and the sequence of the human alpha 2 calcium channel  
disclosed by Wei et al. (AF042792)

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SEQ_ID_N1.se
AF042792.seq                                GCCAGCGCTGC
                                           10

SEQ_ID_N1.se
AF042792.seq  AGGGAGATAGCAGCGCGCAGCCCGCAGAGGCGCTGCGGCCCCGTGCAGCCCCGGAGGCCCC
                20      30      40      50      60      70

SEQ_ID_N1.se
AF042792.seq  TCGCGGAGAAGGCGGCGGCGGAGGAGAGGCCGAGTTACCGCCCGCCGCCCGCGCCCCCCC
                80      90     100     110     120     130

                               10      20      30
SEQ_ID_N1.se                               ATGGCGGTGCCGGCTCGGACCTGCGGCGCC
                               |||||
AF042792.seq  TCCCCGCGGCGCCGCATCTTGAATGGAAACATGGCGGTGCCGGCTCGGACCTGCGGCGCC
                140     150     160     170     180     190

                40      50      60      70      80      90
SEQ_ID_N1.se  TCTCGGCCCCGCCCCAGCGCGGACTGCGCGCCCCCTGGCCCCGGCTGCGGCCCCCACCCTGGC
                |||||
AF042792.seq  TCTCGGCCCCGCCCCAGCGCGGACTGCGCGCCCCCTGGCCCCGGCTGCGGCCCCCACCCTGGC
                200     210     220     230     240     250

                100     110     120     130     140     150
SEQ_ID_N1.se  CCCGGCACCCGCGCGCCGACGTCCGGGCCCCCGCGCCCCGCTGTGGCTGCTGCTGCCGCTT
                |||||
AF042792.seq  CCCGGCACCCGCGCGCCGACGTCCGGGCCCCCGCGCCCCGCTGTGGCTGCTGCTGCCGCTT
                260     270     280     290     300     310

                160     170     180     190     200     210
SEQ_ID_N1.se  CTACCGCTGCTCGCCGCCCCCGGCGCCTCTGCCTACAGCTTCCCCCAGCAGCACACGATG
                |||||
AF042792.seq  CTACCGCTGCTCGCCGCCCCCGGCGCCTCTGCCTACAGCTTCCCCCAGCAGCACACGATG
                320     330     340     350     360     370

                220     230     240     250     260     270
SEQ_ID_N1.se  CAGCACTGGGCCCCGGCGTCTGGAGCAGGAGTTCGACGGCGTGATGCGGATTTTGGAGGC
                |||||
AF042792.seq  CAGCACTGGGCCCCGGCGTCTGGAGCAGGAGTTCGACGGCGTGATGCGGATTTTGGAGGC
                380     390     400     410     420     430

                280     290     300     310     320     330
SEQ_ID_N1.se  GTCCAGCAGCTCCGTGAGATTTACAAGGACAACCGGAACCTGTTTCGAGGTACAGGAGAAT
                |||||
AF042792.seq  GTCCAGCAGCTCCGTGAGATTTACAAGGACAACCGGAACCTGTTTCGAGGTACAGGAGAAT
                440     450     460     470     480     490

                340     350     360     370     380     390
SEQ_ID_N1.se  GAGCCTCAGAAGTTGGTGGAGAAGGTGGCAGGGGACATTGAGAGCCTTCTGGACAGGAAG
                |||||
AF042792.seq  GAGCCTCAGAAGTTGGTGGAGAAGGTGGCAGGGGACATTGAGAGCCTTCTGGACAGGAAG
                500     510     520     530     540     550

                400     410     420     430     440     450
SEQ_ID_N1.se  GTGCAGGCCCTGAAGAGACTGGCTGATGCTGCAGAGAACTTCCAGAAAGCACACCGCTGG
                |||||
AF042792.seq  GTGCAGGCCCTGAAGAGACTGGCTGATGCTGCAGAGAACTTCCAGAAAGCACACCGCTGG
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	560	570	580	590	600	610
	460	470	480	490	500	510
SEQ_ID_N1.se	CAGGACAACATCAAGGAGGAAGACATCGTGTACTATGACGCCAAGGCTGACGCTGAGCTG					
AF042792.seq	CAGGACAACATCAAGGAGGAAGACATCGTGTACTATGACGCCAAGGCTGACGCTGAGCTG					
	620	630	640	650	660	670
	520	530	540	550	560	570
SEQ_ID_N1.se	GACGACCCTGAGAGTGAGGATGTGGAAAGGGGGTCTAAGGCCAGCACCCCTAAGGCTGGAC					
AF042792.seq	GACGACCCTGAGAGTGAGGATGTGGAAAGGGGGTCTAAGGCCAGCACCCCTAAGGCTGGAC					
	680	690	700	710	720	730
	580	590	600	610	620	630
SEQ_ID_N1.se	TTCATCGAGGACCCAACTTCAAGAACAAGGTCAACTATTCATACGCGGCTGTACAGATC					
AF042792.seq	TTCATCGAGGACCCAACTTCAAGAACAAGGTCAACTATTCATACGCGGCTGTACAGATC					
	740	750	760	770	780	790
	640	650	660	670	680	690
SEQ_ID_N1.se	CCTACGGACATCTACAAAGGCTCCACTGTCATCCTCAATGAGCTCAACTGGACAGAGGCC					
AF042792.seq	CCTACGGACATCTACAAAGGCTCCACTGTCATCCTCAATGAGCTCAACTGGACAGAGGCC					
	800	810	820	830	840	850
	700	710	720	730	740	750
SEQ_ID_N1.se	CTGGAGAATGTGTTTCATGGAAAACCGCAGACAAGACCCCACTGCTGTGGCAGGTCTTC					
AF042792.seq	CTGGAGAATGTGTTTCATGGAAAACCGCAGACAAGACCCCACTGCTGTGGCAGGTCTTC					
	860	870	880	890	900	910
	760	770	780	790	800	810
SEQ_ID_N1.se	GGCAGCGCCACAGGAGTCACTCGCTACTACCCGGCCACCCCGTGGCGAGCCCCAAGAAG					
AF042792.seq	GGCAGCGCCACAGGAGTCACTCGCTACTACCCGGCCACCCCGTGGCGAGCCCCAAGAAG					
	920	930	940	950	960	970
	820	830	840	850	860	870
SEQ_ID_N1.se	ATCGACCTGTACGATGTCCGAAGGAGACCCTGGTATATCCAGGGGGCCTCGTCACCCAAA					
AF042792.seq	ATCGACCTGTACGATGTCCGAAGGAGACCCTGGTATATCCAGGGGGCCTCGTCACCCAAA					
	980	990	1000	1010	1020	1030
	880	890	900	910	920	930
SEQ_ID_N1.se	GACATGGTCATCATCGTGGATGTGAGTGGCAGTGTGAGCGGCCTGACCCTGAAGCTGATG					
AF042792.seq	GACATGGTCATCATCGTGGATGTGAGTGGCAGTGTGAGCGGCCTGACCCTGAAGCTGATG					
	1040	1050	1060	1070	1080	1090
	940	950	960	970	980	990
SEQ_ID_N1.se	AAGACATCTGTCTGCGAGATGCTGGACACGCTGTCTGATGATGACTATGTGAATGTGGCC					
AF042792.seq	AAGACATCTGTCTGCGAGATGCTGGACACGCTGTCTGATGATGACTATGTGAATGTGGCC					
	1100	1110	1120	1130	1140	1150
	1000	1010	1020	1030	1040	1050
SEQ_ID_N1.se	TCGTTCAACGAGAAGGCACAGCCTGTGTCATGCTTCACACACCTGGTGCAGGCCAATGTG					
AF042792.seq	TCGTTCAACGAGAAGGCACAGCCTGTGTCATGCTTCACACACCTGGTGCAGGCCAATGTG					
	1160	1170	1180	1190	1200	1210
	1060	1070	1080	1090	1100	1110
SEQ_ID_N1.se	CGCAACAAGAAGGTGTTCAAGGAAGCTGTGCAGGGCATGGTGGCCAAGGGCACCACAGGC					
AF042792.seq	CGCAACAAGAAGGTGTTCAAGGAAGCTGTGCAGGGCATGGTGGCCAAGGGCACCACAGGC					
	1220	1230	1240	1250	1260	1270



	1120	1130	1140	1150	1160	1170
SEQ_ID_N1.se	TACAAGGCCGGCTTTGAGTATGCCTTTGACCAGCTGCAGAACTCCAACATCACTCGGGCC					
AF042792.seq	TACAAGGCCGGCTTTGAGTATGCCTTTGACCAGCTGCAGAACTCCAACATCACTCGGGCC					
	1280	1290	1300	1310	1320	1330
SEQ_ID_N1.se	AACTGCAACAAGATGATCATGATGTTACGGATGGTGGTGAGGACCGCGTGCAGGACGTC					
AF042792.seq	AACTGCAACAAGATGATCATGATGTTACGGATGGTGGTGAGGACCGCGTGCAGGACGTC					
	1340	1350	1360	1370	1380	1390
SEQ_ID_N1.se	TTTGAGAAGTACAATTGGCCAAACCGGACGGTGCGCGTGTCTTTACTTTCTCCGTGGGGCAG					
AF042792.seq	TTTGAGAAGTACAATTGGCCAAACCGGACGGTGCGCGTGTCTTTACTTTCTCCGTGGGGCAG					
	1400	1410	1420	1430	1440	1450
SEQ_ID_N1.se	CATAACTATGACGTCACACCGCTGCAGTGGATGGCCTGTGCCAACAAAGGCTACTATTTT					
AF042792.seq	CATAACTATGACGTCACACCGCTGCAGTGGATGGCCTGTGCCAACAAAGGCTACTATTTT					
	1460	1470	1480	1490	1500	1510
SEQ_ID_N1.se	GAGATCCCTTCCATCGGAGCCATCCGCATCAACACACAGGAATATCTAGATGTGTTGGGC					
AF042792.seq	GAGATCCCTTCCATCGGAGCCATCCGCATCAACACACAGGAATATCTAGATGTGTTGGGC					
	1520	1530	1540	1550	1560	1570
SEQ_ID_N1.se	AGGCCCATGGTGCTGGCAGGCAAGGAGGCCAAGCAGGTTTCAGTGGACCAACGTGTATGAG					
AF042792.seq	AGGCCCATGGTGCTGGCAGGCAAGGAGGCCAAGCAGGTTTCAGTGGACCAACGTGTATGAG					
	1580	1590	1600	1610	1620	1630
SEQ_ID_N1.se	GATGCACTGGGACTGGGGTTGGTGGTAACAGGGACCCTCCCTGTTTTCAACCTGACACAG					
AF042792.seq	GATGCACTGGGACTGGGGTTGGTGGTAACAGGGACCCTCCCTGTTTTCAACCTGACACAG					
	1640	1650	1660	1670	1680	1690
SEQ_ID_N1.se	GATGGCCCTGGGGAAAAGAAGAACCCAGCTGATCCTGGGCGTGATGGGCATTGACGTGGCT					
AF042792.seq	GATGGCCCTGGGGAAAAGAAGAACCCAGCTGATCCTGGGCGTGATGGGCATTGACGTGGCT					
	1700	1710	1720	1730	1740	1750
SEQ_ID_N1.se	CTGAATGACATCAAGAGGCTGACCCCCAACTACACGCTTGGAGCCAACGGCTATGTGTTT					
AF042792.seq	CTGAATGACATCAAGAGGCTGACCCCCAACTACACGCTTGGAGCCAACGGCTATGTGTTT					
	1760	1770	1780	1790	1800	1810
SEQ_ID_N1.se	GCCATTGACCTGAACGGCTACGTGTTGCTGCACCCCAATCTCAAGCCCAGACCACCAAC					
AF042792.seq	GCCATTGACCTGAACGGCTACGTGTTGCTGCACCCCAATCTCAAGCCCAGACCACCAAC					
	1820	1830	1840	1850	1860	1870
SEQ_ID_N1.se	TTCCGGGAGCCTGTGACTCTGGACTTCCTGGATGCGGAGCTAGAGGATGAGAACAAGGAA					
AF042792.seq	TTCCGGGAGCCTGTGACTCTGGACTTCCTGGATGCGGAGCTAGAGGATGAGAACAAGGAA					
	1880	1890	1900	1910	1920	1930

	1780	1790	1800	1810	1820	1830
SEQ_ID_N1.se	GAGATCCGTCGGAGCATGATTGATGGCAACAAGGGCCACAAGCAGATCAGAACGTTGGTC					
AF042792.seq	GAGATCCGTCGGAGCATGATTGATGGCAACAAGGGCCACAAGCAGATCAGAACGTTGGTC					
	1940	1950	1960	1970	1980	1990

	1840	1850	1860	1870	1880	1890
SEQ_ID_N1.se	AAGTCCCTGGATGAGAGGTACATAGATGAGGTGACACGGAACCTACACCTGGGTGCCTATA					
AF042792.seq	AAGTCCCTGGATGAGAGGTACATAGATGAGGTGACACGGAACCTACACCTGGGTGCCTATA					
	2000	2010	2020	2030	2040	2050

	1900	1910	1920	1930	1940	1950
SEQ_ID_N1.se	AGGAGCACTAACTACAGCCTGGGGCTGGTGCTCCCACCCTACAGCACCTTCTACCTCCAA					
AF042792.seq	AGGAGCACTAACTACAGCCTGGGGCTGGTGCTCCCACCCTACAGCACCTTCTACCTCCAA					
	2060	2070	2080	2090	2100	2110

	1960	1970	1980	1990	2000	2010
SEQ_ID_N1.se	GCCAATCTCAGTGACCAGATCCTGCAGGTCAAGTATTTTGAGTTCCTGCTCCCCAGCAGC					
AF042792.seq	GCCAATCTCAGTGACCAGATCCTGCAGGTCAAGTATTTTGAGTTCCTGCTCCCCAGCAGC					
	2120	2130	2140	2150	2160	2170

	2020	2030	2040	2050	2060	2070
SEQ_ID_N1.se	TTTGAGTCTGAAGGACACGTTTTTCATTGCTCCCAGAGAGTACTGCAAGGACCTGAATGCC					
AF042792.seq	TTTGAGTCTGAAGGACACGTTTTTCATTGCTCCCAGAGAGTACTGCAAGGACCTGAATGCC					
	2180	2190	2200	2210	2220	2230

	2080	2090	2100	2110	2120	2130
SEQ_ID_N1.se	TCAGACAACAACACCGAGTTCCTGAAAACTTTATTGAGCTCATGGAGAAAGTGACTCCA					
AF042792.seq	TCAGACAACAACACCGAGTTCCTGAAAACTTTATTGAGCTCATGGAGAAAGTGACTCCA					
	2240	2250	2260	2270	2280	2290

	2140	2150	2160	2170	2180	2190
SEQ_ID_N1.se	GACTCCAAGCAGTGCAACAACCTTCCTTCTGCACAACCTGATCTTGGACACGGGCATCACG					
AF042792.seq	GACTCCAAGCAGTGCAACAACCTTCCTTCTGCACAACCTGATCTTGGACACGGGCATCACG					
	2300	2310	2320	2330	2340	2350

	2200	2210	2220	2230	2240	2250
SEQ_ID_N1.se	CAGCAGCTGGTAGAGCGTGTGTGGAGGGACCAGGATCTCAACACGTACAGCCTACTGGCC					
AF042792.seq	CAGCAGCTGGTAGAGCGTGTGTGGAGGGACCAGGATCTCAACACGTACAGCCTACTGGCC					
	2360	2370	2380	2390	2400	2410

	2260	2270	2280	2290	2300	2310
SEQ_ID_N1.se	GTGTTGCTGCCACAGACGGTGGCATCACCCGAGTCTTCCCCAACAAGGCAGCTGAGGAC					
AF042792.seq	GTGTTGCTGCCACAGACGGTGGCATCACCCGAGTCTTCCCCAACAAGGCAGCTGAGGAC					
	2420	2430	2440	2450	2460	2470

	2320	2330	2340	2350	2360	2370
SEQ_ID_N1.se	TGGACAGAGAACCCTGAGCCCTTCAATGCCAGCTTCTACCGCCGAGCCTGGATAACCAC					
AF042792.seq	TGGACAGAGAACCCTGAGCCCTTCAATGCCAGCTTCTACCGCCGAGCCTGGATAACCAC					
	2480	2490	2500	2510	2520	2530

	2380	2390	2400	2410	2420	2430
SEQ_ID_N1.se	GGTTATGTCTTCAAGCCCCACACCAGGATGCCCTGTTAAGGCCGCTGGAGCTGGAGAAT					
AF042792.seq	GGTTATGTCTTCAAGCCCCACACCAGGATGCCCTGTTAAGGCCGCTGGAGCTGGAGAAT					
	2540	2550	2560	2570	2580	2590

	2440	2450	2460	2470	2480	2490
SEQ_ID_N1.se	GACACTGTGGGCATCCTCGTCAGCACAGCTGTGGAGCTCAGCCTAGGCAGGCGCACACTG					
AF042792.seq	GACACTGTGGGCATCCTCGTCAGCACAGCTGTGGAGCTCAGCCTAGGCAGGCGCACACTG					
	2600	2610	2620	2630	2640	2650

	2500	2510	2520	2530	2540	2550
SEQ_ID_N1.se	AGGCCAGCAGTGGTGGGCGTCAAGCTGGACCTAGAGGCTTGGGCTGAGAAGTTCAAGGTG					
AF042792.seq	AGGCCAGCAGTGGTGGGCGTCAAGCTGGACCTAGAGGCTTGGGCTGAGAAGTTCAAGGTG					
	2660	2670	2680	2690	2700	2710

	2560	2570	2580	2590	2600	2610
SEQ_ID_N1.se	CTAGCCAGCAACCGTACCCACCAAGACCAGCCTCAGAAGTGCGGCCCCAACAGCCACTGT					
AF042792.seq	CTAGCCAGCAACCGTACCCACCAAGACCAGCCTCAGAAGTGCGGCCCCAACAGCCACTGT					
	2720	2730	2740	2750	2760	2770

	2620	2630	2640	2650	2660	2670
SEQ_ID_N1.se	GAGATGGACTGCGAGGTTAACAATGAGGACTTACTCTGTGTCCTCATTGATGATGGAGGA					
AF042792.seq	GAGATGGACTGCGAGGTTAACAATGAGGACTTACTCTGTGTCCTCATTGATGATGGAGGA					
	2780	2790	2800	2810	2820	2830

	2680	2690	2700	2710	2720	2730
SEQ_ID_N1.se	TTCCTGGTGCTGTCAAACCAGAACCATCAGTGGGACCAGGTGGGCAGGTTCTTCAGTGAG					
AF042792.seq	TTCCTGGTGCTGTCAAACCAGAACCATCAGTGGGACCAGGTGGGCAGGTTCTTCAGTGAG					
	2840	2850	2860	2870	2880	2890

	2740	2750	2760	2770	2780	2790
SEQ_ID_N1.se	GTGGATGCCAACCTGATGCTGGCACTCTACAATAACTCCTTCTACACCCGCAAGGAGTCC					
AF042792.seq	GTGGATGCCAACCTGATGCTGGCACTCTACAATAACTCCTTCTACACCCGCAAGGAGTCC					
	2900	2910	2920	2930	2940	2950

	2800	2810	2820	2830	2840	2850
SEQ_ID_N1.se	TATGACTATCAGGCAGCCTGTGCCCCCTCAGCCCCCTGGCAACCTGGGTGCTGCACCCCGG					
AF042792.seq	TATGACTATCAGGCAGCCTGTGCCCCCTCAGCCCCCTGGCAACCTGGGTGCTGCACCCCGG					
	2960	2970	2980	2990	3000	3010

	2860	2870	2880	2890	2900	2910
SEQ_ID_N1.se	GGTGTCTTTGTGCCCACCGTTGCAGATTTCTTAACCTGGCCTGGTGGACCTCTGCTGCC					
AF042792.seq	GGTGTCTTTGTGCCCACCGTTGCAGATTTCTTAACCTGGCCTGGTGGACCTCTGCTGCC					
	3020	3030	3040	3050	3060	3070

	2920	2930	2940	2950	2960	2970
SEQ_ID_N1.se	GCCTGGTCCCTGTTCCAGCAGCTTCTCTACGGCCTCATCTACCACAGCTGGTTCCAAGCA					
AF042792.seq	GCCTGGTCCCTGTTCCAGCAGCTTCTCTACGGCCTCATCTACCACAGCTGGTTCCAAGCA					
	3080	3090	3100	3110	3120	3130

	2980	2990	3000	3010	3020	3030
SEQ_ID_N1.se	GACCCCGCGGAGGCCGAGGGGAGCCCCGAGACGCGGAGAGCAGCTGCGTCATGAAACAG					
AF042792.seq	GACCCCGCGGAGGCCGAGGGGAGCCCCGAGACGCGGAGAGCAGCTGCGTCATGAAACAG					
	3140	3150	3160	3170	3180	3190

	3040	3050	3060	3070	3080	3090
SEQ_ID_N1.se	ACCCAGTACTACTTCGGCTCGGTAAACGCCTCCTACAACGCCATCATCGACTGCGGAAAC					
AF042792.seq	ACCCAGTACTACTTCGGCTCGGTAAACGCCTCCTACAACGCCATCATCGACTGCGGAAAC					
	3200	3210	3220	3230	3240	3250

	3100	3110	3120	3130	3140	3150
SEQ_ID_N1.se	TGCTCCAGGCTGTTCCACGCGCAGAGACTGACCAACACCAATCTTCTCTTTGTGGTGGCC					
AF042792.seq	TGCTCCAGGCTGTTCCACGCGCAGAGACTGACCAACACCAATCTTCTCTTTGTGGTGGCC					
	3260	3270	3280	3290	3300	3310

	3160	3170	3180			
SEQ_ID_N1.se	GAGAAGCCGCTGTGCAGCCAGTGCGAGGCTGGCCGG					
AF042792.seq	GAGAAGCCGCTGTGCAGCCAGTGCGAGGCTGGCCGGCTGCTGCAGAAGGAGACGCACTGC					
	3320	3330	3340	3350	3360	3370

SEQ_ID_N1.se						
AF042792.seq	CCAGCGGACGGCCCGGAGCAGTGTGAGCTAGTGCAGAGACCGGATACCGGAGAGGCCCG					
	3380	3390	3400	3410	3420	3430

SEQ_ID_N1.se						
AF042792.seq	CACATCTGCTTCGACTACAACGCGACAGAAGATACCTCAGACTGTGGCC					
	3440	3450	3460	3470	3480	

SEQ_ID_N1.se						
AF042792.seq	GCGGGGCTCCTTCCCGCCGTCGCTGGGCGTCCTGGTCTCCCTGCAACTGCTGCTCCTCC					
	3490	3500	3510	3520	3530	3540

SEQ_ID_N1.se						
AF042792.seq	TGGGCCTGCCGCCCCGGCCGAGCCTCAAGTCCTCGTCCACGCCTCTCGCCGCCTCTGAG					
	3550	3560	3570	3580	3590	3600

SEQ_ID_N1.se						
AF042792.seq	CACCCTGCCCCACCCACCTCCACTCCCACCTACCCGGCCTCTTCGCCTTTCCACCCCT					
	3610	3620	3630	3640	3650	3660

SEQ_ID_N1.se						
AF042792.seq	CCTGCCCCACACTCCCCGCCTTAGAGCCTCGTCCCTCCCTCACTGAAGGACCTGAGCTGG					
	3670	3680	3690	3700	3710	3720

SEQ_ID_N1.se						
AF042792.seq	CCAGGCCCTGAGAGTCTGGTCTGCGCCTTGGGATGGGGAGTCCCAAAGCGGGACGCCGCA					
	3730	3740	3750	3760	3770	3780

SEQ_ID_N1.se						
AF042792.seq	GGTGTGTTGGCACCCAAATCACATCTCACCTCCGAACTGTTCAAGTGTCCTCCAGACCCTTC					
	3790	3800	3810	3820	3830	3840

SEQ_ID_N1.se						
AF042792.seq	TTGCCTGCTGGGCTCCCCCAGTGGGATGGGACAGGGAGGCCACACGCACTGGTGCCAAA					
	3850	3860	3870	3880	3890	3900

SEQ_ID_N1.se						
AF042792.seq	ACCAGGCCTCTGCTGCCGCCCTTCCTGGAGGCTGCCTATGTTGGGGGGGACCCTGCCTCA					
	3910	3920	3930	3940	3950	3960

SEQ_ID_N1.se						
AF042792.seq	GCTGACCCGGCCTCTCTGCCCCACCCAAGCCCAAACCTGGTTTCTGTGAGAATAGTGGAG					

3970 3980 3990 4000 4010 4020

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AF042792.seq GAAGGTGAGATGGCCAGTTTGAAGCCTGTGCCTCCCAGCTTAAATCCTAGCAGGAGAGAG  
4030 4040 4050 4060 4070 4080

SEQ\_ID\_N1.se

AF042792.seq GCTCTGGGGCAGCCCCCATGGGCTCCTGCCCCTTTCAGGCCTACAGCCACATCCCCAAGC  
4090 4100 4110 4120 4130 4140

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AF042792.seq CCACCAGGTGTCAGGATAGTCACAGTGATAACAGTTCAGACACTACCCCATATACACCTG  
4150 4160 4170 4180 4190 4200

SEQ\_ID\_N1.se

AF042792.seq GAACATTGAGGATGGAACTGGACTCACATTCGACATACCCCACTGGGCACACGCACAAA  
4210 4220 4230 4240 4250 4260

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AF042792.seq CACACACACTATGGGGTGGGGTGGGTGTAGGGGCTTACAAAGCCTTACACAGGGCGAGGG  
4270 4280 4290 4300 4310 4320

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AF042792.seq GTTGGTGGGAGGGTTGGCACCTGCACACTCCATCTCCTGCTCACCACCTGCCTCTAATCT  
4330 4340 4350 4360 4370 4380

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AF042792.seq GAGCTGCAGCCTGGCTGGTCCTCCCATTCTCTAAAGCTGAATGTCAAACAGTGCCAAATGC  
4390 4400 4410 4420 4430 4440

SEQ\_ID\_N1.se

AF042792.seq TGGGGCAGGGGTGAAGAACCCTCTGTCCCACCCCTAGCCACCAGTGTCTCTCAAGTGCC  
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AF042792.seq CCCTCACCTCTCCAGGTGCTCATTGTAACCATTCTCTACTAGTGTGAGGCCCCAGTGGG  
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AF042792.seq ACCACATGCCACTGCCTGCACCTTTCGGCAGAGGAACCCCCACCAGACATCACCTTTGC  
4570 4580 4590 4600 4610 4620

SEQ\_ID\_N1.se

AF042792.seq CTTAGCAGGGGTGACTTTGTCTCTCCTGGCTGGGCCATCCTTCCGCCAATCTGGCCCTTA  
4630 4640 4650 4660 4670 4680

SEQ\_ID\_N1.se

AF042792.seq CACACTCAGGCCTGTGCCCCACTCCCTATCTCCTTCCCACCCCTACACACACACTCCCTGC  
4690 4700 4710 4720 4730 4740

SEQ\_ID\_N1.se

AF042792.seq TTGCAGGAGGCCAACTGTCCCTCCCTTGCTGAACACACACACACACACACACAGG  
4750 4760 4770 4780 4790 4800

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AF042792.seq TGGGGACTGGGCACAGCTCTTCACACCATTTCATTCTGGTCATTTCCCCCAAAGGCATCCC  
4810 4820 4830 4840 4850 4860

SEQ\_ID\_N1.se

AF042792.seq AGCCTGGGGGCCAGTGGGGAAGTGGGGCAAGGGGATATAGTGATGGGGCTCAGATGGAC  
4870 4880 4890 4900 4910 4920

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AF042792.seq TGGGAGGAGGGGGAGGGTGATGCATTAATTAATGGCTTCGTTAATTAATGTCATGTTGCT  
4930 4940 4950 4960 4970 4980

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AF042792.seq TGTCGCTTTCTCAGTGTGTGTGTGTGGTCCATGCCCACTGCTGGTGCCAGGGTGGGTGTC  
4990 5000 5010 5020 5030 5040

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AF042792.seq CATGTGCACCCGGCCTGGATGCCAGCTGTGTCTTCGGGGGCGTGCCTGTAAGTGTAGTG  
5050 5060 5070 5080 5090 5100

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AF042792.seq TAGTCAGGTGCTCAATGGAGAATATAAACATATACAGAAAAATATATATTTTAAGTTTAA  
5110 5120 5130 5140 5150 5160

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AF042792.seq AAAACAGAAAAACAGACAAAACAATCCCCATCAGGTAGCTGTCTAACCCCCAGCTGGGTC  
5170 5180 5190 5200 5210 5220

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AF042792.seq TAATCCTTCTCATTACCCACCCGACCTGGCTGCCCCCTCACCTTGGGCTGGGGGACTGGGG  
5230 5240 5250 5260 5270 5280

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AF042792.seq GGCCATTCCTTTTCTCTGCCCTTTTTTTGTTGTTCTATTTTGTACAGACAAGTTGGAAA  
5290 5300 5310 5320 5330 5340

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AF042792.seq AACACAGCGACAAAAAGTCAAGAACTTTGTAAAATATCGTGTGTGTGATTCCTTGTA  
5350 5360 5370 5380 5390 5400

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AF042792.seq AAATATTTTCAAATGGTTTATTACAGAAGATCAGTTATTAAATAATGTTTCATATTTTCAC  
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AF042792.seq TTC